

Reply and Amendment
U.S. Serial No. 09/341,105
Attorney Reference: 015837-0275805
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linkage map was constructed. Fourteen markers were scorable and polymorphic in this population. The resulting map contains 12 markers in two linkage groups spanning 90 Cm and two unlinked markers (see Fig. 2). The physical location of each marker was established by fluorescent in situ hybridization (FISH). Preliminary results with four markers allowed the assignment of one linkage group to the long arm of the Z chromosome, and one to the short arm.

See the attached Appendix for the changes made to effect the above paragraph.

IN THE CLAIMS:

Please enter the following amended claims:

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1. (Amended) An isolated Z-chromosomal marker DNA selected from the group consisting of Sequence 1 (43.Seq), Sequence 2 (71.Seq), Sequence 3 (80.Seq), Sequence 4 (81.Seq), Sequence 5 (131.Seq), Sequence 6 (147.Seq), Sequence 7 (166.Seq), Sequence 8 (196.Seq), Sequence 9 (199.Seq), Sequence 10 (204.Seq), Sequence 11 (235.Seq), Sequence 12 (249.Seq), Sequence 13 (258.Seq), Sequence 14 (290.Seq), Sequence 15 (309.Seq), Sequence 16 (341.Seq), Sequence 17 (398.Seq), Sequence 18 (420.Seq), and Sequence 19 (435.Seq).

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3. (Amended) A method of using at least one Z-chromosomal marker DNA according to Claim 1 for genetic mapping.

4. (Amended) The method of Claim 3, wherein the genetic mapping is effected to construct a Z-chromosome specific microsatellite linkage map.

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6. (Amended) The method of Claim 4, wherein said at least one Z-chromosomal marker DNA is used to construct a second Z-chromosome specific microsatellite linkage map, and the two maps are compared in order to identify gross chromosomal rearrangements.